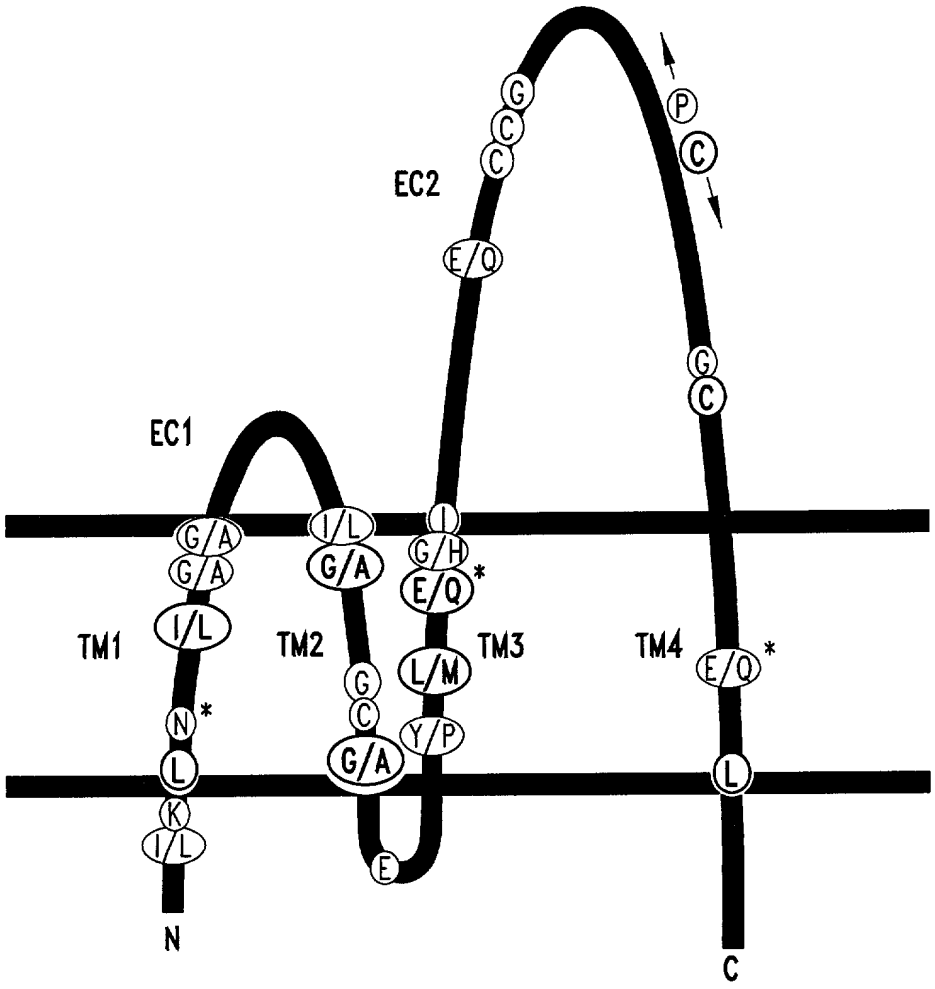

Fig. 1

```
  1  CTTCCTCGGC CGAGCCGGGC CGCGCGGCCG CTGCCGCCGC CGCGCGCGGA
     GAAGGAGCCG GCTCGGCCCG GCGCGCCGGC GACGGCGGCG GCGCGCGCCT

 +1                  ]-----------------------------------
 51  TTCTGCTTCT CAGAAGATGC ACTATTATAG ATACTCTAAC GCCAAAGTCA
     AAGACGAAGA GTCTTCTACG TGATAATATC TATGAGATTG CGGTTTCAGT

 +1 ----------------------------------------------------
101  GCTGCTGGTA CAAGTACCTC CTTTTCAGCT ACAACATCAT CTTCTGGTTG
     CGACGACCAT GTTCATGGAG GAAAAGTCGA TGTTGTAGTA GAAGACCAAC
 -3                                    <------------------

 +3                                 ]---------------------
 +1 ----------------------------------------------------
151  GCTGGAGTTG TCTTCCTTGG AGTCGGGCTG TGGGCATGGA GCGAAAAGGG
     CGACCTCAAC AGAAGGAACC TCAGCCCGAC ACCCGTACCT CGCTTTTCCC
 -3 ----------------------------------------------------

 +3 ----------------------------------------------------
 +1 ----------------------------------------------------
201  TGTGCTGTCC GACCTCACCA AAGTGACCCG GATGCATGGA ATCGACCCTG
     ACACGACAGG CTGGAGTGGT TTCACTGGGC CTACGTACCT TAGCTGGGAC
 -3 ----------------------------------------------------

 +3 ----------------------------------------------------
 +1 ----------------------------------------------------
251  TGGTGCTGGT CCTGATGGTG GGCGTGGTGA TGTTCACCCT GGGGTTCGCC
     ACCACGACCA GGACTACCAC CCGCACCACT ACAAGTGGGA CCCCAAGCGG
 -3 ----------------------------------------------------

 +3 ----------------------------------------------------
 +1 ----------------------------------------------------
301  GGCTGCGTGG GGGCTCTGCG GGAGAATATC TGCTTGCTCA ACTTTTTCTG
     CCGACGCACC CCCGAGACGC CCTCTTATAG ACGAACGAGT TGAAAAAGAC
 -3 ----------------------------------------------------

 +3 ----------------------------------------------------
 +1 ----------------------------------------------------
351  TGGCACCATC GTGCTCATCT TCTTCCTGGA GCTGGCTGTG GCCGTGCTGG
     ACCGTGGTAG CACGAGTAGA AGAAGGACCT CGACCGACAC CGGCACGACC
```

Fig. 2A

```
  +3 ----------------------------------------------------
  +1 ----------------------------------------------------
401  CCTTCCTGTT CCAGGACTGG GTGAGGGACC GGTTCCGGGA GTTCTTCGAG
     GGAAGGACAA GGTCCTGACC CACTCCCTGG CCAAGGCCCT CAAGAAGCTC
  -3 ----------------------------------------------------

  +3 ----------------------------------------------------
  +1 ----------------------------------------------------
                                  ClaI
                                  ~~~~~~~
451  AGCAACATCA AGTCCTACCG GGACGATATC GATCTGCAAA ACCTCATCGA
     TCGTTGTAGT TCAGGATGGC CCTGCTATAG CTAGACGTTT TGGAGTAGCT
  -3 -------[

  +3 --------------->
  +1 ----------------------------------------------------
501  CTCCCTTCAG AAAGCTAACC AGTGCTGTGG CGCATATGGC CCTGAAGACT
     GAGGGAAGTC TTTCGATTGG TCACGACACC GCGTATACCG GGACTTCTGA

  +1 ----------------------------------------------------
551  GGGACCTCAA CGTCTACTTC AATTGCAGCG GTGCCAGCTA CAGCCGAGAG
     CCCTGGAGTT GCAGATGAAG TTAACGTCGC CACGGTCGAT GTCGGCTCTC

  +1 ----------------------------------------------------
601  AAGTGCGGGG TCCCCTTCTC CTGCTGCGTG CCAGATCCTG CGCAAAAAGT
     TTCACGCCCC AGGGGAAGAG GACGACGCAC GGTCTAGGAC GCGTTTTTCA

  +1 ----------------------------------------------------
651  TGTGAACACA CAGTGTGGAT ATGATGTCAG GATTCAGCTG AAGAGCAAGT
     ACACTTGTGT GTCACACCTA TACTACAGTC CTAAGTCGAC TTCTCGTTCA

  +1 ----------------------------------------------------
701  GGGATGAGTC CATCTTCACG AAAGGCTGCA TCCAGGCGCT GGAAAGCTGG
     CCCTACTCAG GTAGAAGTGC TTTCCGACGT AGGTCCGCGA CCTTTCGACC

  +1 ----------------------------------------------------
751  CTCCCGCGGA ACATTTACAT TGTGGCTGGC GTCTTCATCG CCATCTCGCT
     GAGGGCGCCT TGTAAATGTA ACACCGACCG CAGAAGTAGC GGTAGAGCGA
  -1                                          <-------------
```

Fig. 2B

```
  +1 ----------------------------------------------------
 801  GTTGCAGATA TTTGGCATCT TCCTGGCAAG GACGCTGATC TCAGACATCG
      CAACGTCTAT AAACCGTAGA AGGACCGTTC CTGCGACTAG AGTCTGTAGC
  -1 ----------------------------------------------------

  +1 ----------------------------------------------------
 851  AGGCAGTGAA GGCCGGCCAT CACTTCTGAG GAGCAGAGTT GAGGGAGCCG
      TCCGTCACTT CCGGCCGGTA GTGAAGACTC CTCGTCTCAA CTCCCTCGGC
  -1 ----------------------------------------------------

 901  AGCTGAGCCA CGCTGGGAGG CCAGAGCCTT TCTCTGCCAT CAGCCCTACG
      TCGACTCGGT GCGACCCTCC GGTCTCGGAA AGAGACGGTA GTCGGGATGC
  -1 ----------------------------------------------------

  +1                                          ]----------
 951  TCCAGAGGGA GAGGAGCCGA CACCCCCAGA GCCAGTGCCC CATCTTAAGC
      AGGTCTCCCT CTCCTCGGCT GTGGGGGTCT CGGTCACGGG GTAGAATTCG
  -1 ----------------------[

  +1 ----------------------------------------------------
1001  ATCAGCGTGA CGTGACCTCT CTGTTTCTGC TTGCTGGTGC TGAAGACCAA
      TAGTCGCACT GCACTGGAGA GACAAAGACG AACGACCACG ACTTCTGGTT

  +1 ----------------------------------------------------
1051  GGGTCCCCCT TGTTACCTGC CCAAACTTGT GACTGCATCC CTCTGGAGTC
      CCCAGGGGGA ACAATGGACG GGTTTGAACA CTGACGTAGG GAGACCTCAG

  +1 ----------------------------------------------------
1101  TACCCAGAGA CAGAGAATGT GTCTTTATGT GGGAGTGGTG ACTCTGAAAG
      ATGGGTCTCT GTCTCTTACA CAGAAATACA CCCTCACCAC TGAGACTTTC
  -1   <--------------------------------------------------

  +1 ----------------------------------------------------
                                                    PstI
                                                    ~~~~
1151  ACAGAGAGGG CTCCTGTGGC TGCCAGGAGG GCTTGACTCA GACCCCCTGC
      TGTCTCTCCC GAGGACACCG ACGGTCCTCC CGAACTGAGT CTGGGGGACG
  -1 ----------------------------------------------------
```

Fig. 2C

```
   +1 ------------------------------------------------------
      Pst1
      ~~
1201  AGCTCAAGCA TGTCTGCAGG ACACCCTGGT CCCYTYTCCA YTGGCWTCCA
      TCGAGTTCGT ACAGACGTCC TGTGGGACCA GGGRARAGGT RACCGWAGGT
   -1 ------------------------------------------------------

   +1 ----------------------------------->
1251  GACATCTGCT TTGGGTCATC CACATCTGTG GGTNGGCCGT GGGTAGAGGG
      CTGTAGACGA AACCCAGTAG GTGTAGACAC CCANCCGGCA CCCATCTCCC
   -1 ------------------------------------------------------

1301  ACCCACAGGC GTGGACAGGG CATCTCTCTC CATCAAGCAA AGCAGCATGG
      TGGGTGTCCG CACCTGTCCC GTAGAGAGAG GTAGTTCGTT TCGTCGTACG
   -1 -----------------------------------------------------[

1351  GGGGCCTTGC CGTAAACGGG AGGCGNGACG TTGGCCC
      CCCCGGAACG GCATTTGCCC TCCGCNCTGC AACCGGG
```


Fig. 2D

```
  1  MHYYRYSNAK VSCWYKYLLF SYNIIFWLAG VVFLGVGLWA WSEKGVLSDL
 51  TKVTRMHGID PVVLVLMVGV VMFTLGFAGC VGALRENICL LNFFCGTIVL
101  IFFLELAVAV LAFLFQDWVR DRFREFFESN IKSYRDDIDL QNLIDSLQKA
151  NQCCGAYGPE DWDLNVYFNC SGASYSREKC GVPFSCCVPD PAQKVVNTQC
201  GYDVRIQLKS KWDESIFTKG CIQALESWLP RNIYIVAGVF IAISLLQIFG
251  IFLARTLISD IEAVKAGHHF
```

Fig. 3

NTSP5:P104	**CHIR22-1**	TGCAGCCTTTCGTGAAGATGGACTC	25 (7-11-7)
NTSP5:P727	**CHIR22-2**	CCCCATGCTGCTTTGCTTGATGGAG	25 (7-11-7)
NTSP5:P285	**CHIR22-3**	GCTCAGCTCGGCTCCCTCAACTC	23 (7-9-7)
NTSP5:P456	**CHIR22-4**	CACAAGTTTGGGCAGGTAACAAGGG	25 (7-11-7)
NTSP5:P395	**CHIR22-5**	AGAGGTCACGTCACGCTGATGCTTA	25 (7-11-7)
NTSP5:P104	**CHIR22-1RC**	CTCAGGTAGAAGTGCTTTCCGACGT	25 (7-11-7)
NTSP5:P727	**CHIR22-2RC**	GAGGTAGTTCGTTTCGTCGTACCCC	25 (7-11-7)
NTSP5:P285	**CHIR22-3RC**	CTCAACTCCCTCGGCTCGACTCG	23 (7-9-7)
NTSP5:P456	**CHIR22-4RC**	GGGAACAATGGACGGGTTTGAACAC	25 (7-11-7)
NTSP5:P395	**CHIR22-5RC**	ATTCGTAGTCGCACTACGCTGGAGA	25 (7-11-7)

Fig. 4

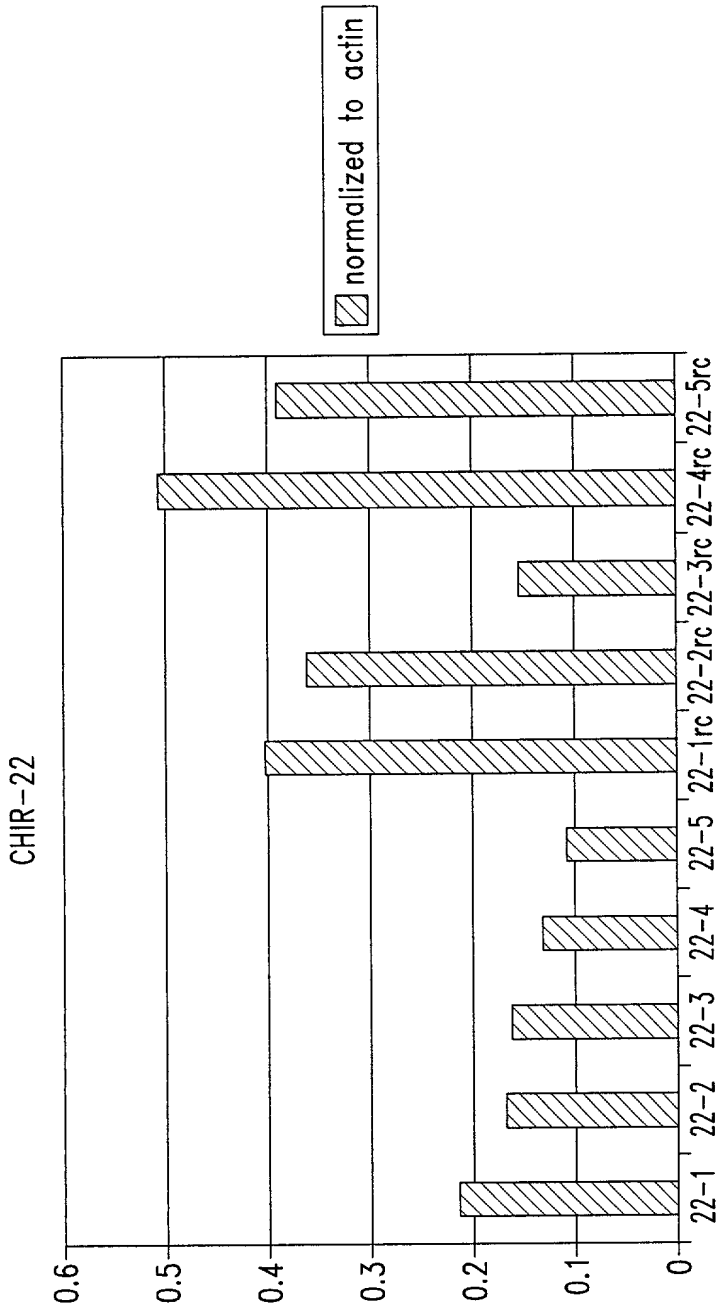
normalized to actin
CHIR-22
0.6
0.5
0.4
0.3
0.2
0.1
0
22-1
22-2
22-3
22-4
22-5
22-1rc
22-2rc
22-3rc
22-4rc
22-5rc

Fig. 5

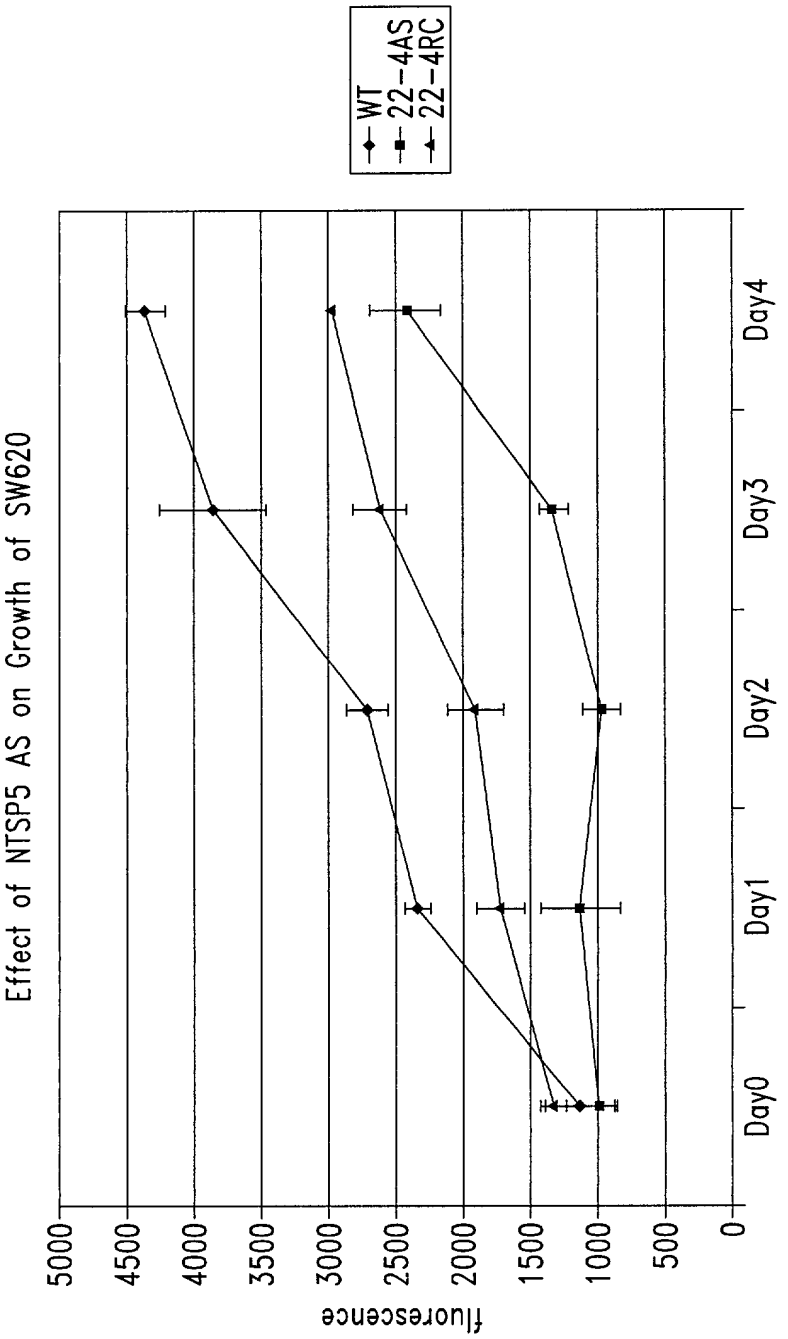
Effect of NTSP5 AS on Growth of SW620
fluorescence
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
Day0
Day1
Day2
Day3
Day4
WT
22-4AS
22-4RC

Fig. 6